



(A)

/home/ru.../carpenda/templ/ss.DNA40370 (1650 bp)

Sequences producing High-scoring Segment Pairs:

		Frame	Score	Match	Pct	E-val
1	P_AAF72416 Human PRO302 cDNA.	+	1650	1650	100	0.0
2	P_AAF30502 Human PRO302 cDNA clone DNA40370-1217.	+	1650	1650	100	0.0
3	P_AAA13199 PRO302, vitellogenin carboxypeptidase ho	+	1650	1650	100	0.0
4	P_AAX52258 Protein PRO302 cDNA clone DNA40370-1217.	+	1650	1650	100	0.0
5	P_AAX25445 Human PRO216 cDNA clone UNQ265.	+	1650	1650	100	0.0
6	AX098272 Sequence 11 from Patent WO0119987.	+	1650	1650	100	0.0
7	NM_021626 Homo sapiens serine carboxypeptidase 1 p	+	1640	1646	100	0.0
8	AF282618 Homo sapiens serine carboxypeptidase 1 p	+	1640	1646	100	0.0
9	AK027373 Homo sapiens cDNA FLJ14467 fis, clone MA	+	1637	1640	100	0.0
10	AF113214 Homo sapiens MSTP034 mRNA, complete cds.	+	1594	1594	100	0.0
11	P_AAC75884 Human ORFX ORF1439 polynucleotide sequen	+	1543	1619	99	0.0

>1 P_AAF72416 Human PRO302 cDNA. (1650 bp) [1 seg]
Score = 1650 (3271 bits), Expect = 0.0
Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/-

```
DNA40370      1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC
*****
P_AAF72416    1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC

DNA40370     61 GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCGTAACGCAGGAGCTGTCATT
*****
P_AAF72416   61 GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCGTAACGCAGGAGCTGTCATT

DNA40370    121 GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
*****
P_AAF72416  121 GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC

DNA40370    181 TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCC
*****
P_AAF72416  181 TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCC

DNA40370    241 CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG
*****
P_AAF72416  241 CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG

DNA40370    301 GAAATTTGGGCCCCCTTGACAGTGATCTCAAACCACGAAAAACACCTGGCTCCAGGCTGCC
*****
P_AAF72416  301 GAAATTTGGGCCCCCTTGACAGTGATCTCAAACCACGAAAAACACCTGGCTCCAGGCTGCC

DNA40370    361 AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCACTTATGTGAATGGTAGTGGT
*****
P_AAF72416  361 AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCACTTATGTGAATGGTAGTGGT

DNA40370    421 GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
*****
P_AAF72416  421 GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC

DNA40370    481 TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCCTATGGA
*****
P_AAF72416  481 TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCCTATGGA

DNA40370    541 GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTTCAGCGAGGGACCATC
*****
P_AAF72416  541 GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTTCAGCGAGGGACCATC

DNA40370    601 AAGTGCACACTTTTGGCGGGGGTTCCTTTGGGTGATTCCTGGATCTCCCTGTGTTGATTCGGT
*****
P_AAF72416  601 AAGTGCACACTTTTGGCGGGGGTTCCTTTGGGTGATTCCTGGATCTCCCTGTGTTGATTCGGT
```

1-A S1MS37 KSA

APR 12 2002

RECEIVED

TECH CENTER 1600/2900

DNA40370	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGCTTGGCAGAG
P_AAF72416	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGCTTGGCAGAG
DNA40370	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
P_AAF72416	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
DNA40370	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAAC TTC
P_AAF72416	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAAC TTC
DNA40370	841	TATAACATCTTAACTAAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
P_AAF72416	841	TATAACATCTTAACTAAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
DNA40370	901	CAGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
P_AAF72416	901	CAGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
DNA40370	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATC
P_AAF72416	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATC
DNA40370	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGT
P_AAF72416	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGT
DNA40370	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
P_AAF72416	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
DNA40370	1141	CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCCTGGGTGCGGAAACTGAAGTGGCCA
P_AAF72416	1141	CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCCTGGGTGCGGAAACTGAAGTGGCCA
DNA40370	1201	GAACTGCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTG
P_AAF72416	1201	GAACTGCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTG
DNA40370	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCCTTGCTTTCTACTGGATTCTGAAAGCT
P_AAF72416	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCCTTGCTTTCTACTGGATTCTGAAAGCT
DNA40370	1321	GGTCATATGGTTCCTTCTGACCAAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
P_AAF72416	1321	GGTCATATGGTTCCTTCTGACCAAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
DNA40370	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
P_AAF72416	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
DNA40370	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGGGCCATTCTTCCCCTGTATCTAACTGGGGCTGT
P_AAF72416	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGGGCCATTCTTCCCCTGTATCTAACTGGGGCTGT
DNA40370	1501	GATCAAGAAGGTTCTTGACCAGCTTCTGCAGAGGATAAAAATCATTGTCTCTGGAGGCAATT
P_AAF72416	1501	GATCAAGAAGGTTCTTGACCAGCTTCTGCAGAGGATAAAAATCATTGTCTCTGGAGGCAATT
DNA40370	1561	TGGAAATTATTTCTGCTTTTAAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTGG
P_AAF72416	1561	TGGAAATTATTTCTGCTTTTAAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTGG

TECH CENTER 1600/2900

APR 12 2002

RECEIVED

BLAST RESULTS A-2

DNA40370 1621 ATCAAAATAAAGGATGATAATAGATATTAA

P_AAF72416 1621 ATCAAAATAAAGGATGATAATAGATATTAA

>2 P_AAF30502 Human PRO302 cDNA clone DNA40370-1217. DNA, PAT 29-MAY-2001 (1650 bp) [1 seg]

Score = 1650 (3271 bits), Expect = 0.0

Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/-

DNA40370 1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC

P_AAF30502 1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC

DNA40370 61 GTCCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCTGAACGCAGGAGCTGTCATT

P_AAF30502 61 GTCCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCTGAACGCAGGAGCTGTCATT

DNA40370 121 GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC

P_AAF30502 121 GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC

DNA40370 181 TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC

P_AAF30502 181 TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC

DNA40370 241 CTGGTCATGTGGCTTCAGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG

P_AAF30502 241 CTGGTCATGTGGCTTCAGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG

DNA40370 301 GAAATTTGGGCCCTTGACAGTGATCTCAAACCACGGAAAACACCTGGCTCCAGGCTGCC

P_AAF30502 301 GAAATTTGGGCCCTTGACAGTGATCTCAAACCACGGAAAACACCTGGCTCCAGGCTGCC

DNA40370 361 AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCACTTATGTGAATGGTAGTGGT

P_AAF30502 361 AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCACTTATGTGAATGGTAGTGGT

DNA40370 421 GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCTGAAGACCTTC

P_AAF30502 421 GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCTGAAGACCTTC

DNA40370 481 TTCAGTTGCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCATATGGA

P_AAF30502 481 TTCAGTTGCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCATATGGA

DNA40370 541 GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTTCAGCGAGGGACCATC

P_AAF30502 541 GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTTCAGCGAGGGACCATC

DNA40370 601 AAGTGCACACTTTGCGGGGGTTGCCTTGGGTGATTCTCGATCTCCCTCTGTTGATTGCGTG

P_AAF30502 601 AAGTGCACACTTTGCGGGGGTTGCCTTGGGTGATTCTCGATCTCCCTCTGTTGATTGCGTG

DNA40370 661 CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTCTCGAAGACAAAGGTCTGGCAGAG

P_AAF30502 661 CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTCTCGAAGACAAAGGTCTGGCAGAG

DNA40370 721 GTGTCTAAGGTTGCAGAGCAAGTACTGAATGUCGTAAATAAGGGGCTCTACAGAGAGGCC

P_AAF30502 721 GTGTCTAAGGTTGCAGAGCAAGTACTGAATGUCGTAAATAAGGGGCTCTACAGAGAGGCC

DNA40370 781 ACAGAGCTCTGGGGGAAAGCAGAAATGATCATTTGAACAGAACACAGATGAGGTGAACCTTC

TECH CENTER 1600/2900

APR 12 2002

BLAST RESULTS A-3


```

*****
P_AAA13199      1 GCCTGTTGETGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGGGGCGCTCTCCC
DNA40370      61 GTCCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
*****
P_AAA13199      61 GTCCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
DNA40370     121 GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
*****
P_AAA13199     121 GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
DNA40370     181 TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
*****
P_AAA13199     181 TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
DNA40370     241 CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCCTAGCACTGGATTGGAACCTTTGAG
*****
P_AAA13199     241 CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCCTAGCACTGGATTGGAACCTTTGAG
DNA40370     301 GAAATTGGGCCCCTTGACAGTGATCTCAAACCACGAAAACCACCTGGCTCCAGGCTGCC
*****
P_AAA13199     301 GAAATTGGGCCCCTTGACAGTGATCTCAAACCACGAAAACCACCTGGCTCCAGCTGCC
DNA40370     361 AGTCTCCTATTTGTGGATAATCCCGTGGGCACCTGGGTTCAGTTATGTGAATGGTAGTG
*****
P_AAA13199     361 AGTCTCCTATTTGTGGATAATCCCGTGGGCACCTGGGTTCAGTTATGTGAATGGTAGTG
DNA40370     421 GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAACCTT
*****
P_AAA13199     421 GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAACCTT
DNA40370     481 TTCAGTTGCCACAAGAATTCAGACAGTTCATTCTACATTTCTCAGAGTCCCTATGGA
*****
P_AAA13199     481 TTCAGTTGCCACAAGAATTCAGACAGTTCATTCTACATTTCTCAGAGTCCCTATGGA
DNA40370     541 GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACGCGAGGGACCATC
*****
P_AAA13199     541 GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACGCGAGGGACCATC
DNA40370     601 AAGTGCAACTTTGCGGGGGTTGCCCTTGGGTGATTCCTGGATCTCCCTGTGATTGCGGTG
*****
P_AAA13199     601 AAGTGCAACTTTGCGGGGGTTGCCCTTGGGTGATTCCTGGATCTCCCTGTGATTGCGGTG
DNA40370     661 CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
*****
P_AAA13199     661 CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
DNA40370     721 GTGTCCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
*****
P_AAA13199     721 GTGTCCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
DNA40370     781 ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTC
*****
P_AAA13199     781 ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTC
DNA40370     841 TATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
*****
P_AAA13199     841 TATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
DNA40370     901 CAGAGCCACCTAGTTTGTCTTTGTGACGGCCACGTGAGACACCTACAACGAGATGCCCTA
*****
P_AAA13199     901 CAGAGCCACCTAGTTTGTCTTTGTGACGGCCACGTGAGACACCTACAACGAGATGCCCTA
DNA40370     961 AGCCAGCTGATGAATGGGTCCTATCAGAAAGAGCTCAAAATTAATTCAGGATCAATCC

```

RECEIVED

BLAST RESULTS A-5

RECEIVED

APR 12 2002

6-A STIM2258

TECH CENTER 1600/2900

```

*****
P_AAA13199 961 AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTTATTCCTGAGGATCAATCC
DNA40370 1021 TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
*****
P_AAA13199 1021 TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
DNA40370 1081 ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
*****
P_AAA13199 1081 ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
DNA40370 1141 CTGGATCTCATCGTAGATACCATGGGTGAGGAGGCCCTGGGTGCGGAAACTGAAGTGGCCA
*****
P_AAA13199 1141 CTGGATCTCATCGTAGATACCATGGGTGAGGAGGCCCTGGGTGCGGAAACTGAAGTGGCCA
DNA40370 1201 GAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG
*****
P_AAA13199 1201 GAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG
DNA40370 1261 GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCCTTGCTTTCTACTGGATTCTGAAAGCT
*****
P_AAA13199 1261 GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCCTTGCTTTCTACTGGATTCTGAAAGCT
DNA40370 1321 GGTTCATATGGTTCCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
*****
P_AAA13199 1321 GGTTCATATGGTTCCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
DNA40370 1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCCTTGGGGCACAGAGCT
*****
P_AAA13199 1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCCTTGGGGCACAGAGCT
DNA40370 1441 GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
*****
P_AAA13199 1441 GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
DNA40370 1501 GATCAAGAAGGTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
*****
P_AAA13199 1501 GATCAAGAAGGTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
DNA40370 1561 TGGAAATTATTTCTGCTTCTTAAAAAAACCTAAGATTTTTTAAAAAAATTGATTTGTTTTG
*****
P_AAA13199 1561 TGGAAATTATTTCTGCTTCTTAAAAAAACCTAAGATTTTTTAAAAAAATTGATTTGTTTTG
DNA40370 1621 ATCAAAATAAAGGATGATAATAGATATTAA
*****
P_AAA13199 1621 ATCAAAATAAAGGATGATAATAGATATTAA

```

>4 P_AAX52258 Protein PRO302 cDNA clone DNA40370-1217. DNA, PAT 25-JUN-1999
(1650 bp) [1 seg]
Score = 1650 (3271 bits), Expect = 0.0
Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/+

```

DNA40370 1 GCCTGTTGCTGATGCTGCCGTGCCGTAATCTGTCATGGAGGTGGCACTGCCGGGCTCTCCC
*****
P_AAX52258 1 GCCTGTTGCTGATGCTGCCGTGCCGTAATCTGTCATGGAGGTGGCACTGCCGGGCTCTCCC
DNA40370 61 GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGCCCTGAACGCAGGAGCTGTGATT
*****
P_AAX52258 61 GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGCCCTGAACGCAGGAGCTGTGATT
DNA40370 121 GACTGGCCACAGAGGAGGGAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
*****
P_AAX52258 121 GACTGGCCACAGAGGAGGGAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC

```

DNA40370	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
P_AAX52258	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
DNA40370	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAACTTTGAG
P_AAX52258	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAACTTTGAG
DNA40370	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACACCTGGCTCCAGGCTGCC
P_AAX52258	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACACCTGGCTCCAGGCTGCC
DNA40370	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCAGTTATGTGAATGGTAGTGGT
P_AAX52258	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCAGTTATGTGAATGGTAGTGGT
DNA40370	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
P_AAX52258	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
DNA40370	481	TCAGTTGCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCATGGA
P_AAX52258	481	TCAGTTGCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCATGGA
DNA40370	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACAGCGAGGGACCATC
P_AAX52258	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACAGCGAGGGACCATC
DNA40370	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTCGGATCTCCCCTGTTGATTCCGGTG
P_AAX52258	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTCGGATCTCCCCTGTTGATTCCGGTG
DNA40370	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
P_AAX52258	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
DNA40370	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
P_AAX52258	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
DNA40370	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAATTC
P_AAX52258	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAATTC
DNA40370	841	TATAACATCTTAAGTAAAAGCACTCCACGCTTACAATGGAGTCGAGTCTAGAATTCACA
P_AAX52258	841	TATAACATCTTAAGTAAAAGCACTCCACGCTTACAATGGAGTCGAGTCTAGAATTCACA
DNA40370	901	CAGAGCCACCTAGTTTGTCTTTGTGACGCGCCACGTGAGACACCTACAACGAGATGCCTTA
P_AAX52258	901	CAGAGCCACCTAGTTTGTCTTTGTGACGCGCCACGTGAGACACCTACAACGAGATGCCTTA
DNA40370	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCTGAGGATCAATCC
P_AAX52258	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCTGAGGATCAATCC
DNA40370	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
P_AAX52258	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
DNA40370	1081	ATTAGCATTTGTGGACGAGTTGCTGGAGGCGATCAACCTGACGGTGTATAATGGACAG
P_AAX52258	1081	ATTAGCATTTGTGGACGAGTTGCTGGAGGCGATCAACCTGACGGTGTATAATGGACAG

BLAST RESULTS A-F

DNA40370 1141 CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCCTGGGTGCGGAACTGAAGTGGCCA
 P_AAX52258 1141 CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCCTGGGTGCGGAACTGAAGTGGCCA

DNA40370 1201 GAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG
 P_AAX52258 1201 GAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG

DNA40370 1261 GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
 P_AAX52258 1261 GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT

DNA40370 1321 GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
 P_AAX52258 1321 GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT

DNA40370 1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
 P_AAX52258 1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT

DNA40370 1441 GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
 P_AAX52258 1441 GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT

DNA40370 1501 GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTTGTCTCTGGAGGCAATT
 P_AAX52258 1501 GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTTGTCTCTGGAGGCAATT

DNA40370 1561 TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTGTGTTTTG
 P_AAX52258 1561 TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTGTGTTTTG

DNA40370 1621 ATCAAAATAAAGGATGATAATAGATATTAA
 P_AAX52258 1621 ATCAAAATAAAGGATGATAATAGATATTAA

>5 P_AAX25445 Human PRO216 cDNA clone UNQ265. (1650 bp) [1 seg]
 Score = 1650 (3271 bits), Expect = 0.0
 Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/-

DNA40370 1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC
 P_AAX25445 1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC

DNA40370 61 GTCCCGCGGTGCTTGTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
 P_AAX25445 61 GTCCCGCGGTGCTTGTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT

DNA40370 121 GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
 P_AAX25445 121 GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC

DNA40370 181 TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCC
 P_AAX25445 181 TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCC

DNA40370 241 CTGGTCATGTGGCTTCAGGCGGTCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG
 P_AAX25445 241 CTGGTCATGTGGCTTCAGGCGGTCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG

DNA40370 301 GAAATTTGGGCCCTTTGACAGTGATCTCAAAACACCGAAAAACCACTGGCTCCAGGCTGCC
 P_AAX25445 301 GAAATTTGGGCCCTTTGACAGTGATCTCAAAACACCGAAAAACCACTGGCTCCAGGCTGCC

BLAST RESULTS A-8

DNA40370	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT
P_AAX25445	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT
DNA40370	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
P_AAX25445	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
DNA40370	481	TTTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCCTATGGA
P_AAX25445	481	TTTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCCTATGGA
DNA40370	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTTCAGCGAGGGACCATC
P_AAX25445	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTTCAGCGAGGGACCATC
DNA40370	601	AAGTGCAACTTTGCGGGGGTTGCCCTGGGTGATTCTCGGATCTCCCCTGTTGATTTCGGTG
P_AAX25445	601	AAGTGCAACTTTGCGGGGGTTGCCCTGGGTGATTCTCGGATCTCCCCTGTTGATTTCGGTG
DNA40370	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
P_AAX25445	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
DNA40370	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
P_AAX25445	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
DNA40370	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAAC TTC
P_AAX25445	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAAC TTC
DNA40370	841	TATAACATCTTAACTAAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
P_AAX25445	841	TATAACATCTTAACTAAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
DNA40370	901	CAGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
P_AAX25445	901	CAGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
DNA40370	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAATTTATTCCTGAGGATCAATCC
P_AAX25445	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAATTTATTCCTGAGGATCAATCC
DNA40370	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
P_AAX25445	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
DNA40370	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
P_AAX25445	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
DNA40370	1141	CTGGATCTCATCGTAGATACCATGGGTGAGGAGGCTGGGTGCGGAAACTGAAGTGGCCA
P_AAX25445	1141	CTGGATCTCATCGTAGATACCATGGGTGAGGAGGCTGGGTGCGGAAACTGAAGTGGCCA
DNA40370	1201	GAAGTGCCTAAATTCAGTCAGCTGAAGTGGAAAGGCCCTGTACAGTGACCTTAAATCTTTG
P_AAX25445	1201	GAAGTGCCTAAATTCAGTCAGCTGAAGTGGAAAGGCCCTGTACAGTGACCTTAAATCTTTG
DNA40370	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
P_AAX25445	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT

BLAST RESULTS A-9

DNA40370 1321 GGTTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
 P_AAX25445 1321 GGTTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT

DNA40370 1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
 P_AAX25445 1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT

DNA40370 1441 GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
 P_AAX25445 1441 GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT

DNA40370 1501 GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
 P_AAX25445 1501 GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT

DNA40370 1561 TGGAAATTATTTCTGCTTCTTAAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG
 P_AAX25445 1561 TGGAAATTATTTCTGCTTCTTAAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG

DNA40370 1621 ATCAAAATAAAGGATGATAATAGATATTAA
 P_AAX25445 1621 ATCAAAATAAAGGATGATAATAGATATTAA

>6 AX098272 Sequence 11 from Patent W00119987. (1650 bp) [1 seg]
 Score = 1650 (3271 bits), Expect = 0.0
 Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/-

DNA40370 1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCCTCTCCC
 AX098272 1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCCTCTCCC

DNA40370 61 GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
 AX098272 61 GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT

DNA40370 121 GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTTATGTGACGGTCCGCAAGGATGCC
 AX098272 121 GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTTATGTGACGGTCCGCAAGGATGCC

DNA40370 181 TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAAGTTCTCAGAAGTGGCC
 AX098272 181 TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAAGTTCTCAGAAGTGGCC

DNA40370 241 CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAAGTCTTGAG
 AX098272 241 CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAAGTCTTGAG

DNA40370 301 GAAATTGGGCCCTTGACAGTGATCTCAAACCACGGAAAACCACTGGCTCCAGGCTGCC
 AX098272 301 GAAATTGGGCCCTTGACAGTGATCTCAAACCACGGAAAACCACTGGCTCCAGGCTGCC

DNA40370 361 AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT
 AX098272 361 AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT

DNA40370 421 GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
 AX098272 421 GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC

DNA40370 481 TTCAGTTGGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGATTCCTATGGA
 AX098272 481 TTCAGTTGGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGATTCCTATGGA

BLAST RESULTS A-10

DNA40370	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTTCAGCGAGGGACCATC *****
AX098272	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTTCAGCGAGGGACCATC *****
DNA40370	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTCGATCTCCCCTGTTGATTTCGGTG *****
AX098272	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTCGATCTCCCCTGTTGATTTCGGTG *****
DNA40370	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG *****
AX098272	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG *****
DNA40370	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC *****
AX098272	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC *****
DNA40370	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAAC TTC *****
AX098272	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAAC TTC *****
DNA40370	841	TATAACATCTTAAC TAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA *****
AX098272	841	TATAACATCTTAAC TAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA *****
DNA40370	901	CAGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTA *****
AX098272	901	CAGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTA *****
DNA40370	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC *****
AX098272	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC *****
DNA40370	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC *****
AX098272	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC *****
DNA40370	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG *****
AX098272	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG *****
DNA40370	1141	CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCA *****
AX098272	1141	CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCA *****
DNA40370	1201	GAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG *****
AX098272	1201	GAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG *****
DNA40370	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT *****
AX098272	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT *****
DNA40370	1321	GGTCATATGTTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT *****
AX098272	1321	GGTCATATGTTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT *****
DNA40370	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT *****
AX098272	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT *****
DNA40370	1441	GAGCTGAGGCGGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT *****
AX098272	1441	GAGCTGAGGCGGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT *****

BLAST RESULTS A-11

BLAST RESULTS A-12

```
DNA40370 1501 GATCAAGAAGGTTCCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
*****
AX098272 1501 GATCAAGAAGGTTCCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
*****
DNA40370 1561 TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTGTGTTTG
*****
AX098272 1561 TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTGTGTTTG
*****
DNA40370 1621 ATCAAAATAAAGGATGATAATAGATATTAA
*****
AX098272 1621 ATCAAAATAAAGGATGATAATAGATATTAA
*****
>7 NM_021626 Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1)
(1921 bp) [1 seg]
Score = 1640 (3251 bits), Expect = 0.0
Identities = 1646/1648 (99%), at 2,1-1649,1648, Strand +/-

DNA40370 2 CCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCG
*****
NM_021626 1 CCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCG
*****
DNA40370 62 TCCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTG
*****
NM_021626 61 TCCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTG
*****
DNA40370 122 ACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCT
*****
NM_021626 121 ACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCT
*****
DNA40370 182 ACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCC
*****
NM_021626 181 ACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCC
*****
DNA40370 242 TGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAGG
*****
NM_021626 241 TGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAGG
*****
DNA40370 302 AAATTGGGCCCCCTTGACAGTGATCTCAAACACGGAAAACACCTGGCTCCAGGCTGCCA
*****
NM_021626 301 AAATTGGGCCCCCTTGACAGTGATCTCAAACACGGAAAACACCTGGCTCCAGGCTGCCA
*****
DNA40370 362 GTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCACTTATGTGAATGGTAGTGGTG
*****
NM_021626 361 GTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCACTTATGTGAATGGTAGTGGTG
*****
DNA40370 422 CCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCTGAAGACCTTCT
*****
NM_021626 421 CCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCTGAAGACCTTCT
*****
DNA40370 482 TCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCATATGGAG
*****
NM_021626 481 TCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCATATGGAG
*****
DNA40370 542 GAAAAATGSCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACGCGAGGGACCATCA
*****
NM_021626 541 GAAAAATGSCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACGCGAGGGACCATCA
*****
DNA40370 602 AGTGCAACTTTGCGGGGGTTGCCCTTGGGTGATTTCCTGGATCTCCCCCTGTTGATTCCGTTG
*****
NM_021626 601 AGTGCAACTTTGCGGGGGTTGCCCTTGGGTGATTTCCTGGATCTCCCCCTGTTGATTCCGTTG
*****
DNA40370 662 TCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTTCTGGCAGAGG
*****
NM_021626 661 TCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTTCTGGCAGAGG
*****
```

DNA40370	722	TGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGGCTCTACAGAGAGGCCA
NM_021626	721	TGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGGCTCTACAGAGAGGCCA
DNA40370	782	CAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCT
NM_021626	781	CAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCT
DNA40370	842	ATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACAC
NM_021626	841	ATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACAC
DNA40370	902	AGAGCCACCTAGTTTGTCTTTGTTCAGCGCCACGTGAGACACCTACAACGAGATGCCCTTAA
NM_021626	901	AGAGCCACCTAGTTTGTCTTTGTTCAGCGCCACGTGAGACACCTACAACGAGATGCCCTTAA
DNA40370	962	GCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCT
NM_021626	961	GCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCT
DNA40370	1022	GGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCA
NM_021626	1021	GGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCA
DNA40370	1082	TTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGC
NM_021626	1081	TTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGC
DNA40370	1142	TGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAG
NM_021626	1141	TGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAG
DNA40370	1202	AACCTGCCTAAATTACAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTGG
NM_021626	1201	AACCTGCCTAAATTACAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTGG
DNA40370	1262	AAACATCTGCTTTTGTCAAGTCCACAAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTG
NM_021626	1261	AAACATCTGCTTTTGTCAAGTCCACAAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTG
DNA40370	1322	GTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTC
NM_021626	1321	GTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTC
DNA40370	1382	AGCAAGAAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTG
NM_021626	1381	AGCAAGAAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTG
DNA40370	1442	AGCTGAGGCGCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTG
NM_021626	1441	AGCTGAGGCGCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTG
DNA40370	1502	ATCAAGAAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
NM_021626	1501	ATCAAGAAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
DNA40370	1562	GGAAATTAATTTCTGCTTCTTAAAAAACCTAAGATTTTAAAAAAATTGATTTGTTTTGA
NM_021626	1561	GGAAATTAATTTCTGCTTCTTAAAAAACCTAAGATTTTAAAAAAATTGATTTGTTTTGA
DNA40370	1622	TCAAAAATAAAGGATGATAATAGATATTA
NM_021626	1621	TCAAAAATAAAGGATGATAATAGATATTA

BLAST RESULTS A-13

>8 AF282618 Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1)
 (1921 bp) [1 seq]
 Score = 1640 (3251 bits), Expect = 0.0
 Identities = 1646/1648 (99%), at 2,1-1649,1648, Strand +/+

DNA40370	2	CCTGTTGCTGATGCTGCCGTGCGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCCG
AF282618	1	CCTGTTGCTGATGCTGCCGTGCGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCCG
DNA40370	62	TCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTG
AF282618	61	TCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTG
DNA40370	122	ACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCT
AF282618	121	ACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCT
DNA40370	182	ACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAAGTCTCAGAAGTGGCCC
AF282618	181	ACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAAGTCTCAGAAGTGGCCC
DNA40370	242	TGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTGAGG
AF282618	241	TGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTGAGG
DNA40370	302	AAATTGGGCCCCCTTGACAGTGATCTCAAACACGGAAAACACCTGGCTCCAGGCTGCCA
AF282618	301	AAATTGGGCCCCCTTGACAGTGATCTCAAACACGGAAAACACCTGGCTCCAGGCTGCCA
DNA40370	362	GTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCAAGTTATGTGAATGGTAGTGGTG
AF282618	361	GTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCAAGTTATGTGAATGGTAGTGGTG
DNA40370	422	CCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCT
AF282618	421	CCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCT
DNA40370	482	TCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCACATTTTCTCAGAGTCCATATGGAG
AF282618	481	TCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCACATTTTCTCAGAGTCCATATGGAG
DNA40370	542	GAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACAGCGAGGGACCATCA
AF282618	541	GAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACAGCGAGGGACCATCA
DNA40370	602	AGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCCCTGGATCTCCCCGTGTTGATTCCGTGC
AF282618	601	AGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCCCTGGATCTCCCCGTGTTGATTCCGTGC
DNA40370	662	TCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGG
AF282618	661	TCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGG
DNA40370	722	TGTC TAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCA
AF282618	721	TGTC TAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCA
DNA40370	782	CAGAGCTGTGGGGGAAAGCAGAAATGATCATGGAACAGAACACAGATGGGGTGAACCTTCT
AF282618	781	CAGAGCTGTGGGGGAAAGCAGAAATGATCATGGAACAGAACACAGATGGGGTGAACCTTCT
DNA40370	842	ATAACATCTTAACTAAAAAGCACTCCGACCTTACAAATGGAGTCGAGTCTAGAATTCACAC

BLAST RESULTS A-A

AF282618 841 ATAACATCTTAACATAAGCACTCCACGCTCTACAATGGAGTCGAGTCTAGAATTCACAC

DNA40370 902 AGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTAA

AF282618 901 AGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTAA

DNA40370 962 GCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCTTGAGGATCAATCCT

AF282618 961 GCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCTTGAGGATCAATCCT

DNA40370 1022 GGGGAGGCCAGGCTACCAACGCTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCA

AF282618 1021 GGGGAGGCCAGGCTACCAACGCTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCA

DNA40370 1082 TTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGC

AF282618 1081 TTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGC

DNA40370 1142 TGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAACTGAAGTGGCCAG

AF282618 1141 TGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAACTGAAGTGGCCAG

DNA40370 1202 AACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTGG

AF282618 1201 AACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTGG

DNA40370 1262 AAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTG

AF282618 1261 AAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTG

DNA40370 1322 GTCATATGGTTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTC

AF282618 1321 GTCATATGGTTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTC

DNA40370 1382 AGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTG

AF282618 1381 AGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTG

DNA40370 1442 AGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTG

AF282618 1441 AGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTG

DNA40370 1502 ATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTT

AF282618 1501 ATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTT

DNA40370 1562 GGAAATTATTTCTGCTTCTTAAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTGA

AF282618 1561 GGAAATTATTTCTGCTTCTTAAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTGA

DNA40370 1622 TCAAAATAAAGGATGATAATAGATATTA

AF282618 1621 TCAAAATAAAGGATGATAATAGATATTA

BLAST RESULTS A-15

>9 AF027373 Homo sapiens cDNA FLJ14467 fis, clone MAMMA1000672, weakly (1641 bp)
[1 seg]

Score = 1637 (3245 bits), Expect = 0.0

Identities = 1640/1641 (99%), at 8,1-1648,1641, Strand +/-

DNA40370 8 GCTGATGCTGCGCTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGC

AF027373 1 GCTGATGCTGCGCTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGC

DNA40370 68 GCTGATGCTGCGCTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGC

```

*****
AK027373      61  GGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGC
DNA40370     128  CCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGT
*****
AK027373     121  CCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGT
DNA40370     188  TCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCCTGGTCA
*****
AK027373     181  TCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCCTGGTCA
DNA40370     248  TGTGGCTTCAGGGCGGTCCAGGCGGTTCAGCACTGGATTTGGAACTTTGAGGAAATTG
*****
AK027373     241  TGTGGCTTCAGGGCGGTCCAGGCGGTTCAGCACTGGATTTGGAACTTTGAGGAAATTG
DNA40370     308  GGCCCCCTTGACAGTGATCTCAAACACGGAACACCTGGCTCCAGGCTGCCAGTCTCC
*****
AK027373     301  GGCCCCCTTGACAGTGATCTCAAACACGGAACACCTGGCTCCAGGCTGCCAGTCTCC
DNA40370     368  TATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGTGCCTATG
*****
AK027373     361  TATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGTGCCTATG
DNA40370     428  CCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTT
*****
AK027373     421  CCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTT
DNA40370     488  GCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAA
*****
AK027373     481  GCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAA
DNA40370     548  TGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGACCATCAAGTGCA
*****
AK027373     541  TGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGACCATCAAGTGCA
DNA40370     608  ACTTTGCGGGGGTTGCCTTGGGTGATTCCCTGGATCTCCCCTGTTGATTCGGTGCTCTCCT
*****
AK027373     601  ACTTTGCGGGGGTTGCCTTGGGTGATTCCCTGGATCTCCCCTGTTGATTCGGTGCTCTCCT
DNA40370     668  GGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTC'TGGCAGAGGTGTCTA
*****
AK027373     661  GGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTC'TGGCAGAGGTGTCTA
DNA40370     728  AGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGC
*****
AK027373     721  AGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGC
DNA40370     788  TGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACA
*****
AK027373     781  TGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACA
DNA40370     843  TCCTAACTAAAAGCACTCCCAAGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCC
*****
AK027373     841  TCCTAACTAAAAGCACTCCCAAGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCC
DNA40370     903  ACCTAAGTTTGTCTTTGTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGC
*****
AK027373     901  ACCTAAGTTTGTCTTTGTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGC
DNA40370     968  TCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCTGGGGAG
*****
AK027373     961  TCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCTGGGGAG
DNA40370    1023  GCGTGGCTACCAAGCTCTTTGTGAACATTCAGGAGGACTTCATGAACCAACTCATTAGCA

```

BLAST RESULTS A-16


```

*****
AK027373 1021 GCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCA
DNA40370 1088 TTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATC
*****
AK027373 1081 TTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATC
DNA40370 1148 TCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAGAAGCTGC
*****
AK027373 1141 TCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAGAAGCTGC
DNA40370 1208 CTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCCTAAATCTTTGGAAACAT
*****
AK027373 1201 CTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCCTAAATCTTTGGAAACAT
DNA40370 1268 CTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATA
*****
AK027373 1261 CTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATA
DNA40370 1328 TGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAG
*****
AK027373 1321 TGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAG
DNA40370 1388 AATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGA
*****
AK027373 1381 AATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGA
DNA40370 1448 GGCCGCTGAAGCTGTAGGAAGCGCCATTCTCCCTGTATCTAACTGGGGCTGTGATCAAG
*****
AK027373 1441 GGCCGCTGAAGCTGTAGGAAGCGCCACTCTCCCTGTATCTAACTGGGGCTGTGATCAAG
DNA40370 1508 AAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAT
*****
AK027373 1501 AAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAT
DNA40370 1568 TATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTGTGTTTGATCAAAA
*****
AK027373 1561 TATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTGTGTTTGATCAAAA
DNA40370 1628 TAAAGGATGATAATAGATATT
*****
AK027373 1621 TAAAGGATGATAATAGATATT

```

>10 AF113214 Homo sapiens MSTP034 mRNA, complete cds. mRNA, PRI 12-DEC-2000 (1902 bp) [1 seg]

Score = 1594 (3160 bits), Expect = 0.0

Identities = 1594/1594 (100%), at 56,1-1649,1594, Strand +/+

```

DNA40370 56 CTCCCGTECCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAAGGAGCTG
*****
AF113214 1 CTCCCGTECCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAAGGAGCTG
DNA40370 116 TCATTGACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGG
*****
AF113214 61 TCATTGACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGG
DNA40370 176 ATGCCTACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAAC
*****
AF113214 121 ATGCCTACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAAC
DNA40370 236 TGCCCTGTTTCATGTGGCTTCAGGGCGGTTCAGGCGGTTCCTAGCACTGATTGGAAGT
*****
AF113214 181 TGCCCTGTTTCATGTGGCTTCAGGGCGGTTCAGGCGGTTCCTAGCACTGATTGGAAGT

```

DNA40370	296	TTGAGGAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGG
AF113214	241	TTGAGGAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGG
DNA40370	356	CTGCCAGTCTCCTATTTGTGGATAATCCCGTGGGCACCTGGGTTTCAGTTATGTGAATGGTA
AF113214	301	CTGCCAGTCTCCTATTTGTGGATAATCCCGTGGGCACCTGGGTTTCAGTTATGTGAATGGTA
DNA40370	416	GTGGTGCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGA
AF113214	361	GTGGTGCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGA
DNA40370	476	CCTTCTTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCT
AF113214	421	CCTTCTTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCT
DNA40370	536	ATGGAGGAAAAATGGCAGCTGGCATTTGGTCTAGAGCTTTATAAGGCCATTTCAGCGAGGGA
AF113214	481	ATGGAGGAAAAATGGCAGCTGGCATTTGGTCTAGAGCTTTATAAGGCCATTTCAGCGAGGGA
DNA40370	596	CCATCAAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCCCTGGATCTCCCCTGTTGATT
AF113214	541	CCATCAAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCCCTGGATCTCCCCTGTTGATT
DNA40370	656	CGGTGCTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGG
AF113214	601	CGGTGCTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGG
DNA40370	716	CAGAGGTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAG
AF113214	661	CAGAGGTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAG
DNA40370	776	AGGCCACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGA
AF113214	721	AGGCCACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGA
DNA40370	836	ACTTCTATAACATCTTAAGTAAAAGCACTCCACGCTCTACAATGGAGTCGAGTCTAGAAT
AF113214	781	ACTTCTATAACATCTTAAGTAAAAGCACTCCACGCTCTACAATGGAGTCGAGTCTAGAAT
DNA40370	896	TCACACAGAGCCACCTAGTTTGTCTTTGTGTCAGCGCCACGTGAGACACCTACAACGAGATG
AF113214	841	TCACACAGAGCCACCTAGTTTGTCTTTGTGTCAGCGCCACGTGAGACACCTACAACGAGATG
DNA40370	956	CCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAAGAAGCTCAAAATTATTCCTGAGGATC
AF113214	901	CCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAAGAAGCTCAAAATTATTCCTGAGGATC
DNA40370	1016	AATCCTGGGGAGGCCAGGCTACCAACCTCTTTGTGAACATGGAGGAGGACTTCATGAAGC
AF113214	961	AATCCTGGGGAGGCCAGGCTACCAACCTCTTTGTGAACATGGAGGAGGACTTCATGAAGC
DNA40370	1076	CAGTCATTAGCATTTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATG
AF113214	1021	CAGTCATTAGCATTTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATG
DNA40370	1136	GACAGCTGGATCTCATCGTAGATACCATGGGTCAAGGAGGCTGGGTGCGGAAACTGAAGT
AF113214	1081	GACAGCTGGATCTCATCGTAGATACCATGGGTCAAGGAGGCTGGGTGCGGAAACTGAAGT
DNA40370	1196	GGCCAGAACTGCCATAAATTCAGTCAGCTGAAGTGGAAAGGCCCTGTACAGTGACCTTAAAT
AF113214	1141	GGCCAGAACTGCCATAAATTCAGTCAGCTGAAGTGGAAAGGCCCTGTACAGTGACCTTAAAT

BLAST RESULTS A-19

DNA40370 1256 CTTTGGAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTTCTACTGGATTCTGA
 AF113214 1201 CTTTGGAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTTCTACTGGATTCTGA
 DNA40370 1316 AAGCTGGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGG
 AF113214 1261 AAGCTGGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGG
 DNA40370 1376 TGACTCAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACA
 AF113214 1321 TGACTCAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACA
 DNA40370 1436 GAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGG
 AF113214 1381 GAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGG
 DNA40370 1496 GCTGTGATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGG
 AF113214 1441 GCTGTGATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGG
 DNA40370 1556 CAATTTGGAAATTATTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTG
 AF113214 1501 CAATTTGGAAATTATTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTG
 DNA40370 1616 TTTTGATCAAAATAAAGGATGATAATAGATATTA
 AF113214 1561 TTTTGATCAAAATAAAGGATGATAATAGATATTA

>11 P_AAC75884 Human ORFX ORF1439 polynucleotide sequence SEQ ID NO:2877. (1921 bp) [1 seg]

Score = 1543 (3059 bits), Expect = 0.0

Identities = 1619/1642 (98%), Gaps = 3/1642 (0%), at 8,2-1649,1640, Strand +/-

DNA40370 8 GCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGC
 P_AAC75884 2 GCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGC
 DNA40370 68 GGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGC
 P_AAC75884 62 GGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGC
 DNA40370 128 CCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCCTACATGT
 P_AAC75884 122 CCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCCTACATGT
 DNA40370 188 TCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCA
 P_AAC75884 182 TCTGGTGGCTCTATTATGCCACC-ACTCCTGCAAGAACT--TCAGAACTGCCCTGGTCA
 DNA40370 248 TGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAGGAAATTG
 P_AAC75884 239 TGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAGGAAATTG
 DNA40370 308 GGCCCTTTGACAGTGATCTCAAACACGGAAACCACTGGCTCCAGGCTGCCAGTCTCC
 P_AAC75884 299 GGCCCTTTGACAGTGATCTCAAACACGGAAACCACTGGCTCCAGGCTGCCAGTCTCC
 DNA40370 368 TATTTGTGGATAATCCCGTGGGCACCTGGGTTTCACTTATGTGAATGGTACTGGTGCCTATG
 P_AAC75884 359 TATTTGTGGATAATCCCGTGGGCACCTGGGTTTCACTTATGTGAATGGTACTGGTGCCTATG
 DNA40370 428 CCAAGGACCTGGCTATGGTGGCTTCAGGACATGATGGTTCTCTCTGAAGACCTCTTCACTT
 P_AAC75884 419 CCAAGGACCTGGCTATGGTGGCTTCAGGACATGATGGTTCTCTCTGAAGACCTCTTCACTT

BLAST RESULTS A-9

DNA40370	488	GCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAA
P_AAC75884	479	GCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAA
DNA40370	548	TGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTTCAGCGAGGGACCATCAAGTGCA
P_AAC75884	539	TGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTTCAGCGAGGGACCATCAAGTGCA
DNA40370	608	ACTTTGCGGGGGTTGCCTTGGGTGATTTCCTGGATCTCCCCTGTTGATTTCGGTGCTCTCCT
P_AAC75884	599	ACTTTGCGGGGGTTGCCTTGGGTGATTTCCTGGATCTCCCCTGTTGATTTCGGTGCTCTCCT
DNA40370	668	GGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTA
P_AAC75884	659	GGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTA
DNA40370	728	AGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGC
P_AAC75884	719	AGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGC
DNA40370	788	TGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACA
P_AAC75884	779	TGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACA
DNA40370	848	TCTTAACATAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCC
P_AAC75884	839	TCTTAACATAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCC
DNA40370	908	ACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGC
P_AAC75884	899	ACCTAGTTTGTCTCTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGC
DNA40370	968	TCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCTGGGGAG
P_AAC75884	959	TCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCTGGGGAG
DNA40370	1028	GCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCA
P_AAC75884	1019	GCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCA
DNA40370	1088	TTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATC
P_AAC75884	1079	TTGTGGATACGTTGCTGGAGGCAGGGGTCAATGTGACTGTGTATAATGGGCAGCTGGATC
DNA40370	1148	TCATCGTAGATACCATGGGTTCAGGAGGCCTGGGTGCGGAAACTGAAGTGCCAGAACTGC
P_AAC75884	1139	TCATTGTGGACACCATAGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGCCAGAACTGT
DNA40370	1208	CTAAATTTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCCTAAATCTTTGGAACAT
P_AAC75884	1199	CCAGATTCAATCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCCTAAATCTTTGGAACAT
DNA40370	1268	CTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATA
P_AAC75884	1259	CTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATA
DNA40370	1328	TGGTTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAG
P_AAC75884	1319	TGGTTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAG
DNA40370	1388	AATAGGATGGATGGGGCTGGAGATGAGCTGCTTTGGCCTTGGGGGACAGAGCTGAGCTGA
P_AAC75884	1379	AATAGGATGGATGGGGCTGGAGATGAGCTGCTTTGGCCTTGGGGGACAGAGCTGAGCTGA

BLAST RESULTS A-20

DNA40370	1448	GGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTGATCAAG

P_AAC75884	1439	GGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTGATCAAG
DNA40370	1508	AAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCCTCTGGAGGCAATTTGGAAAT

P_AAC75884	1499	AAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCCTCTGGAGGCAATTTGGAAAT
DNA40370	1568	TATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTGATCAAAA

P_AAC75884	1559	TATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTGATCAAAA
DNA40370	1628	TAAAGGATGATAATAGATATTA

P_AAC75884	1619	TAAAGGATGATAATAGATATTA

BLAST RESULTS A-21



(B)

Tue Jul 25:23 2001 [BLASTP 2.1.3 [Apr-1-2001], NCBI]
/home/ruby/va/Melbzo/carpenti/templ/pl.DNA40370 (452 aa)

Sequences producing High-scoring Segment Pairs:

		Score	Match	Pct	E-val
1	E_AAB80255 Human PFO302 protein - Homo sapiens.	2382	452	100	0.0
2	E_AAB20341 Human PFO302 - Homo sapiens.	2382	452	100	0.0
3	F_AAY88378 PFO302, vitellogenic carboxypeptidase hom	2382	452	100	0.0
4	F_AAY13387 protein PFO302 - Homo sapiens.	2382	452	100	0.0
5	F_AAY95768 Human PFO302 (vitellogenic carboxypeptida	2382	452	100	0.0
6	AAG16642.1 serine carboxypeptidase 1 precursor prote	2382	452	100	0.0
7	NP_067639.1 serine carboxypeptidase 1 precursor prote	2382	452	100	0.0
8	P_AAB41675 Human ORFX ORF1439 polypeptide sequence S	2306	439	97	0.0
9	AAG39285.1 MSTP034 - Homo sapiens	2116	402	100	0.0

>1 P_AAB80255 Human PFO302 protein - Homo sapiens. (452 aa) [1 seg]

Score = 2382 (922 bits), Expect = 0.0

Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

```
DNA40370      1 MELALFFSPVFFWLLLLLELLLSLNAGAVIDWPTEEGKEVWDYVTVFKDAYMFWWLYYATN
*****
P_AAB80255    1 MELALFFSPVFFWLLLLLELLLSLNAGAVIDWPTEEGKEVWDYVTVFKDAYMFWWLYYATN

DNA40370     61 SCKNFSELEPLVMWLQGGFSGSSTGFGNFEEIGPLDSCLKPRKTTWLQAASLIFVDNPVGT
*****
P_AAB80255    61 SCKNFSELEPLVMWLQGGFSGSSTGFGNFEEIGPLDSCLKPRKTTWLQAASLIFVDNPVGT

DNA40370    121 GFCYVIESGAYAKDLAMVASDMVLLKTFESCHKEFQTVPFYIFSESYGGRMAAGIGLEL
*****
P_AAB80255   121 GFCYVIESGAYAKDLAMVASDMVLLKTFESCHKEFQTVPFYIFSESYGGRMAAGIGLEL

DNA40370    161 YKAIQFGTIEKNFAAGVALSDSWISPVISVLSWGPILYSMSLLEDRGLAEVSEFAEQVLNA
*****
P_AAB80255   161 YKAIQFGTIEKNFAAGVALSDSWISPVISVLSWGPILYSMSLLEDRGLAEVSEFAEQVLNA

DNA40370    241 VNEGILREATRELWGKAEMITEQNTDGVNFYNIITKSTPTSTMESLSLEFQSHLVCLQQRH
*****
P_AAB80255   241 VNEGILREATRELWGKAEMITEQNTDGVNFYNIITKSTPTSTMESLSLEFQSHLVCLQQRH

DNA40370    301 VERHLQFDALSQIMNSPIEFELHIIPEIQSWGGQATNVFVNMEEDENKPVISIVDELLEAG
*****
P_AAB80255   301 VERHLQFDALSQIMNSPIEFELHIIPEIQSWGGQATNVFVNMEEDENKPVISIVDELLEAG

DNA40370    361 INVTYVNGQLDINVDTMGQEAWVERKLEWPELPKFSQLKWKALYSDPKSLETSAFVKSYKN
*****
P_AAB80255   361 INVTYVNGQLDINVDTMGQEAWVERKLEWPELPKFSQLKWEALYSDPKSLETSAFVKSYKN

DNA40370    421 LAFYWLKAGKRVFSDQGIKALKMMKRLVTQQE
*****
P_AAB80255   421 LAFYWLKAGKRVFSDQGIKALKMMKRLVTQQE
```

>2 P_AAB20341 Human PFO302 - Homo sapiens. (452 aa) [1 seg]

Score = 2382 (922 bits), Expect = 0.0

Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

```
DNA40370      1 MELALFFSPVFFWLLLLLELLLSLNAGAVIDWPTEEGKEVWDYVTVFKDAYMFWWLYYATN
```

BLAST RESULTS B-1

```

*****
P_AAB70341      1 MELALFFSPVPRWLLLLPLLLGLNAGAVIDWPTEEGFEVWDYVTVRKEAYMFWWLYYATN
      DNA40370      61 SCNFSESELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGT
*****
P_AAB70341      61 SCNFSESELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGT
      DNA40370     121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVFFYIFSES YGGKMAAGIGLEL
*****
P_AAB70341     121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVFFYIFSES YGGKMAAGIGLEL
      DNA40370     181 YFAIQETIEKCNFAGVALGDSWISPVDSVLSWGPYLYSMALLEDKGLAEVSKVAEQVLNA
*****
P_AAB70341     181 YFAIQETIEKCNFAGVALGDSWISPVDSVLSWGPYLYSMALLEDKGLAEVSKVAEQVLNA
      DNA40370     241 VHKGLFEATELWGFKAEMIIEQNTDGVNFYNILTKSTPTSTNESSLEFTQSHLVCLCQRH
*****
P_AAB70341     241 VHKGLFEATELWGFKAEMIIEQNTDGVNFYNILTKSTPTSTNESSLEFTQSHLVCLCQRH
      DNA40370     301 VFHLQFDALSQLMNGPIEFKKLIIIEFDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG
*****
P_AAB70341     301 VFHLQFDALSQLMNGPIEFKKLIIIEFDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG
      DNA40370     361 INVTVINGQLDELVDITMGQEAWVERELFWPELPEFSQLEWHALYSDFESLETSAFVKSYKN
*****
P_AAB70341     361 INVTVINGQLDELVDITMGQEAWVERELFWPELPEFSQLEWHALYSDFESLETSAFVKSYKN
      DNA40370     421 LAFTWLIKAGHIVPEDQGMALKMNRIVTQDE
*****
P_AAB70341     421 LAFTWLIKAGHIVPEDQGMALKMNRIVTQDE

```

>3 P_AAY88378 PF0307, v tellogenic carboxypeptidase homologue amino acid
sequence - Homo sapiens. (451 aa) [1 seq]
Score = 2382 (922 bit), Expect = 0.0
Identities = 42/451 (93%), Positives = 452/452 (100%), at 1,1-452,452

```

      DNA40370      1 MELALFFSPVPRWLLLLPLLLGLNAGAVIDWPTEEGFEVWDYVTVRKEAYMFWWLYYATN
*****
P_AAY88378      1 MELALFFSPVPRWLLLLPLLLGLNAGAVIDWPTEEGFEVWDYVTVRKEAYMFWWLYYATN
      DNA40370      61 SCNFSESELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGT
*****
P_AAY88378      61 SCNFSESELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGT
      DNA40370     121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVFFYIFSES YGGKMAAGIGLEL
*****
P_AAY88378     121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVFFYIFSES YGGKMAAGIGLEL
      DNA40370     181 YFAIQETIEKCNFAGVALGDSWISPVDSVLSWGPYLYSMALLEDKGLAEVSKVAEQVLNA
*****
P_AAY88378     181 YFAIQETIEKCNFAGVALGDSWISPVDSVLSWGPYLYSMALLEDKGLAEVSKVAEQVLNA
      DNA40370     241 VHKGLFEATELWGFKAEMIIEQNTDGVNFYNILTKSTPTSTNESSLEFTQSHLVCLCQRH
*****
P_AAY88378     241 VHKGLFEATELWGFKAEMIIEQNTDGVNFYNILTKSTPTSTNESSLEFTQSHLVCLCQRH
      DNA40370     301 VFHLQFDALSQLMNGPIEFKKLIIIEFDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG
*****
P_AAY88378     301 VFHLQFDALSQLMNGPIEFKKLIIIEFDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG

```

BLAST RESULTS B-2

BLAST RESULTS B-3

```

*****
P_AAY88378 301 VRHLQFLALSQLMNGPIRKKLKIIPEIQSWGQATNVFVNMEEDFMKPVISIVDELLEAG
DNA40370 361 INVTVYNGQLDLIVDTMGQEAWVEKLEWPELPKFSQKWKALYSDFKSLETSFAFKSYKH
*****
P_AAY88378 361 INVTVYNGQLDLIVDTMGQEAWVEKLEWPELPKFSQKWKALYSDFKSLETSFAFKSYKH
DNA40370 411 LAFYWILEAGHMVPSDQGMALKNMRLVTQQE
*****
P_AAY88378 411 LAFYWILEAGHMVPSDQGMALKNMRLVTQQE

```

>4 P_AAY13387 protein PF0302 - Homo sapiens. (452 aa) [1 seg]
 Score = 2382 (922 bits), Expect = 0.0
 Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

```

DNA40370 1 MELALFEESPVPFWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVFEDAYMFWWLYYATH
*****
P_AAY13387 1 MELALFEESPVPFWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVFEDAYMFWWLYYATH
DNA40370 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSCLKPKKTTWLQAASLLFVDNPVGT
*****
P_AAY13387 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSCLKPKKTTWLQAASLLFVDNPVGT
DNA40370 121 GESYVNGSGAYAKDLAMVASDMNVLLFTFFSCHKEFQTVPFYIFSLFYGGKMAAGIGLEL
*****
P_AAY13387 121 GESYVNGSGAYAKDLAMVASDMNVLLFTFFSCHKEFQTVPFYIFSLFYGGKMAAGIGLEL
DNA40370 181 YEALQEGTIKCNFAGVALQDSWLSPVLSVLSWGPYLYSMILLEDFGLAEVSKVAEQVLNA
*****
P_AAY13387 181 YEALQEGTIKCNFAGVALQDSWLSPVLSVLSWGPYLYSMILLEDFGLAEVSKVAEQVLNA
DNA40370 241 VNEGLYEATEIWGFAEMIIEQNTDGVNFYNIILTESTPTSTNESSLEFTQSHLVCLCQRI
*****
P_AAY13387 241 VNEGLYEATEIWGFAEMIIEQNTDGVNFYNIILTESTPTSTNESSLEFTQSHLVCLCQRI
DNA40370 301 VRHLQEDALSQIMNGPIRKKLKIIPEIQSWGQATNVFVNMEEDFMKPVISIVDELLEAG
*****
P_AAY13387 301 VRHLQEDALSQIMNGPIRKKLKIIPEIQSWGQATNVFVNMEEDFMKPVISIVDELLEAG
DNA40370 361 INVTVYNGQLDLIVDTMGQEAWVEKLEWPELPKFSQKWKALYSDFKSLETSFAFKSYKH
*****
P_AAY13387 361 INVTVYNGQLDLIVDTMGQEAWVEKLEWPELPKFSQKWKALYSDFKSLETSFAFKSYKH
DNA40370 411 LAFYWILEAGHMVPSDQGMALKNMRLVTQQE
*****
P_AAY13387 411 LAFYWILEAGHMVPSDQGMALKNMRLVTQQE

```

>5 P_AAY05768 Human PKnox1 (vitellogenin carboxypeptidase homologue) - Homo (452 aa) [1 seg]
 Score = 2382 (922 bits), Expect = 0.0
 Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

```

DNA40370 1 MELALFEESPVPFWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVFEDAYMFWWLYYATH
*****
P_AAY13387 1 MELALFEESPVPFWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVFEDAYMFWWLYYATH
DNA40370 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSCLKPKKTTWLQAASLLFVDNPVGT

```



```

*****
P_AAY05768 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKFRKTTWLQAASLLFVONPVGT
DNA40370 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL
*****
P_AAY05768 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL
DNA40370 181 YKATQPGTIRKCNFAGVALGDSWISFVLSVLSWGFYLYSMSLLEDKGLAEVSKVAEQVLNA
*****
P_AAY05768 181 YKATQPGTIRKCNFAGVALGDSWISFVLSVLSWGFYLYSMSLLEDKGLAEVSKVAEQVLNA
DNA40370 241 VNKGLYFEATELWGFARMII EQNTIGVNFYNI LTKSTPTSTMESSLEFTQSHLVCLCQRH
*****
P_AAY05768 241 VNKGLYFEATELWGFARMII EQNTIGVNFYNI LTKSTPTSTMESSLEFTQSHLVCLCQRH
DNA40370 301 VEHLQFDALSQIMNGPIEFELKIIIFELQSWGGQATNVFVNMEEDFMKPVISIVDEILLEAG
*****
P_AAY05768 301 VEHLQFDALSQIMNGPIEFELKIIIFELQSWGGQATNVFVNMEEDFMKPVISIVDEILLEAG
DNA40370 361 INVTVYNGQLDLIVDTMGQEAWVFLKWPPELPEFSQLKWKALYSDPKSLETSAFVKSYKN
*****
P_AAY05768 361 INVTVYNGQLDLIVDTMGQEAWVFLKWPPELPEFSQLKWKALYSDPKSLETSAFVKSYKN
DNA40370 421 LAFYWLKAGHMVPCDQGMALIMMRENTQQE
*****
P_AAY05768 421 LAFYWLKAGHMVPCDQGMALIMMRENTQQE

```

>6 AAG16692.1 serine carboxypeptidase 1 precursor protein - Homo sapiens (452 aa) [1 seq]
 Score = 2382 (922 bits), Expect = 0.0
 Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

```

DNA40370 1 MELALRESFVPEWLLILPLILLGLNAGAVIDWPTTEEGKEVWDYVTVRKDAYNFWWLYYATN
*****
AAG16692.1 1 MELALRESFVPEWLLILPLILLGLNAGAVIDWPTTEEGKEVWDYVTVRKDAYNFWWLYYATN
DNA40370 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKFRKTTWLQAASLLFVONPVGT
*****
AAG16692.1 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKFRKTTWLQAASLLFVONPVGT
DNA40370 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL
*****
AAG16692.1 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL
DNA40370 181 YKATQPGTIRKCNFAGVALGDSWISFVLSVLSWGFYLYSMSLLEDKGLAEVSKVAEQVLNA
*****
AAG16692.1 181 YKATQPGTIRKCNFAGVALGDSWISFVLSVLSWGFYLYSMSLLEDKGLAEVSKVAEQVLNA
DNA40370 241 VNKGLYFEATELWGFARMII EQNTIGVNFYNI LTKSTPTSTMESSLEFTQSHLVCLCQRH
*****
AAG16692.1 241 VNKGLYFEATELWGFARMII EQNTIGVNFYNI LTKSTPTSTMESSLEFTQSHLVCLCQRH
DNA40370 301 VEHLQFDALSQIMNGPIEFELKIIIFELQSWGGQATNVFVNMEEDFMKPVISIVDEILLEAG
*****
AAG16692.1 301 VEHLQFDALSQIMNGPIEFELKIIIFELQSWGGQATNVFVNMEEDFMKPVISIVDEILLEAG
DNA40370 361 INVTVYNGQLDLIVDTMGQEAWVFLKWPPELPEFSQLKWKALYSDPKSLETSAFVKSYKN
*****
AAG16692.1 361 INVTVYNGQLDLIVDTMGQEAWVFLKWPPELPEFSQLKWKALYSDPKSLETSAFVKSYKN

```

```

*****
AAG16692.1 361 INVTVYNGQLDLIVDTMGQEAWVEKLEKWPPELPKFSQLEKWKALYSDPKSLETSFVKS YKN
      DNA40370 421 LAFYWILKAGHMVPSDQGMALKMMPLVTQGE
      *****
AAG16692.1 411 LAFYWILKAGHMVPSDQGMALKMMELVTQGE

```

>7 NP_067639.1 serine carboxypeptidase 1 precursor protein - Homo sapiens (452 aa) [1 seq]

Score = 2382 (922 bits), Expect = 0.0

Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

```

      DNA40370 1 MELALHESPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
      *****
NP_067639.1 1 MELALHESPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN

      DNA40370 61 SCKNEFELPLVMWLQGGPGGSSSTGPGNFEEIGPLDSULKPEKTTWLQAASLLFVDNIPVGT
      *****
NP_067639.1 61 SCKNEFELPLVMWLQGGPGGSSSTGPGNFEEIGPLDSULKPEKTTWLQAASLLFVDNIPVGT

      DNA40370 121 GFSYVDSGAYAKDLAMVAEDMMVLLKTFEFSCHKEEQTVPEYIFSESYGKMAAGIGLEL
      *****
NP_067639.1 111 GFSYVDSGAYAKDLAMVAEDMMVLLKTFEFSCHKEEQTVPEYIFSESYGKMAAGIGLEL

      DNA40370 181 YKATQFGTIKCNFAGVALGDSWIKPVLCVLCWGPYLYSMELLEDKGLAEVSKVAEQVLNA
      *****
NP_067639.1 181 YKATQFGTIKCNFAGVALGDSWIKPVLCVLCWGPYLYSMELLEDKGLAEVSKVAEQVLNA

      DNA40370 241 VNEGLYFEATELWGEKAMMIEQNTDGVNHFYNIILTESTPTSTHESSELEFQSHLVCLCQRH
      *****
NP_067639.1 241 VNEGLYFEATELWGEKAMMIEQNTDGVNHFYNIILTESTPTSTHESSELEFQSHLVCLCQRH

      DNA40370 301 VEHLQFQALSQIMNGEIERFKLKIIEIDQSWGGQATNVFVNMEEDFMKEFVISIVDELLEAG
      *****
NP_067639.1 301 VEHLQFQALSQIMNGEIERFKLKIIEIDQSWGGQATNVFVNMEEDFMKEFVISIVDELLEAG

      DNA40370 361 INVTVYNGQLDLIVDTMGQEAWVEKLEKWPPELPKFSQLEKWKALYSDPKSLETSFVKS YKN
      *****
NP_067639.1 361 INVTVYNGQLDLIVDTMGQEAWVEKLEKWPPELPKFSQLEKWKALYSDPKSLETSFVKS YKN

      DNA40370 421 LAFYWILKAGHMVPSDQGMALKMMELVTQGE
      *****
NP_067639.1 411 LAFYWILKAGHMVPSDQGMALKMMELVTQGE

```

>8 P_AAB41675 Human ORFX ORF144 polypeptide sequence SEQ ID NO: 873 - Homo (451 aa) [1 seq]

Score = 2506 (892 bits), Expect = 0.0

Identities = 449/452 (99%), Positives = 444/452 (98%), Gaps = 1/452 (0%), at 1,1-452,451

```

      DNA40370 1 MELALHESPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
      *****
P_AAB41675 1 MELALHESPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN

      DNA40370 61 SCKNEFELPLVMWLQGGPGGSSSTGPGNFEEIGPLDSULKPEKTTWLQAASLLFVDNIPVGT
      *****
P_AAB41675 61 SCKNEFELPLVMWLQGGPGGSSSTGPGNFEEIGPLDSULKPEKTTWLQAASLLFVDNIPVGT

```

DNA40370 121 GFSYVNGSGAYAKDLAMVASDMMVLLLTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL
 P_AAB41675 120 GFSYVNGSGAYAKDLAMVASDMMVLLLTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL

DNA40370 181 YFAIQPGTIFCNFAGVALGDSWISPVDSVLSWGPYLYSMGLLEDKGLAEVSEVAEQVLNA
 P_AAB41675 180 YFAIQPGTIFCNFAGVALGDSWISPVDSVLSWGPYLYSMGLLEDKGLAEVSEVAEQVLNA

DNA40370 241 VNKGlyFEATELWGFaEMIIEQNTDGVNfYNIILTKSTPTSTMESSLEFTQSHLVCLCQRH
 P_AAB41675 240 VNKGlyFEATELWGFaEMIIEQNTDGVNfYNIILTKSTPTSTMESSLEFTQSHLVCLCQRH

DNA40370 301 VEHLQFDALSQLMNGPIRKELKIIFEDQSWGGQATNVFVIMEEDFMKPVISIVDELLEAG
 P_AAB41675 300 VEHLQFDALSQLMNGPIRKELKIIFEDQSWGGQATNVFVIMEEDFMKPVIDIVDTLLEAG

DNA40370 361 INVTVYNGQLDLIVDTMGQEAWVRKLEWPELPKFSQLEKWKALYSDEPKSLETSAFVKSYKN
 P_AAB41675 360 INVTVYNGQLDLIVDTMGQEAWVRKLEWPELSEFNQLKWKALYSDEPKSLETSAFVKSYKN

DNA40370 411 LAFTYWLKAGEMVPSDQGLMAKKMRLVTDQE
 P_AAB41675 410 LAFTYWLKAGEMVPSDQGLMAKKMRLVTDQE

>9 AAG39285.1 M1TP034 - Homo sapiens 407 aa [1 seg]
 Score = 2116 (319 bits), Expect = 0.0
 Identities = 402/402 (100%), Positives = 402/402 (100%), at 51,1-452,402

DNA40370 51 MFWWLYYATNESCNESELI VMWLQGGPGGSGTGFGHPEEIGPLISDLKPKRTTWLQAAS
 AAG39285.1 1 MFWWLYYATNESCNESELI VMWLQGGPGGSGTGFGHPEEIGPLISDLKPKRTTWLQAAS

DNA40370 111 LLEFVQNPVGTFFSYVNGSGAYAKDLAMVASDMMVLLLTFFSCHKEFQTVPFYIFSES YGG
 AAG39285.1 61 LLEFVQNPVGTFFSYVNGSGAYAKDLAMVASDMMVLLLTFFSCHKEFQTVPFYIFSES YGG

DNA40370 181 KMAAG! GLELYKALQPGTIFCNFAGVALGDSWISPVDSVLSWGPYLYSMGLLEDKGLAEV
 AAG39285.1 111 KMAAG! GLELYKALQPGTIFCNFAGVALGDSWISPVDSVLSWGPYLYSMGLLEDKGLAEV

DNA40370 241 SEVAEQVLNAVNHGLYREATELWGFaEMIIEQNTDGVNfYNIILTKSTPTSTMESSLEFTQ
 AAG39285.1 181 SEVAEQVLNAVNHGLYREATELWGFaEMIIEQNTDGVNfYNIILTKSTPTSTMESSLEFTQ

DNA40370 301 SHLVCLCQFELVEHLQFDALSQLMNGPIRKELKIIFEDQSWGGQATNVFVIMEEDFMKPVISIVDELLEAG
 AAG39285.1 241 SHLVCLCQFELVEHLQFDALSQLMNGPIRKELKIIFEDQSWGGQATNVFVIMEEDFMKPVISIVDELLEAG

DNA40370 361 INVTVYNGQLDLIVDTMGQEAWVRKLEWPELPKFSQLEKWKALYSDEPKSLETSAFVKSYKN
 AAG39285.1 361 INVTVYNGQLDLIVDTMGQEAWVRKLEWPELSEFNQLKWKALYSDEPKSLETSAFVKSYKN

DNA40370 411 LAFTYWLKAGEMVPSDQGLMAKKMRLVTDQE
 AAG39285.1 411 LAFTYWLKAGEMVPSDQGLMAKKMRLVTDQE

BLAST RESULTS B-6